

## SEQUENCE LISTING

<110> Schnorr, Kirk Matthew  
Christensen, Lars Lehmann Hylling

<120> Fungal carbohydrate-binding module

<130> 10499.204-US

<160> 9

<170> PatentIn version 3.3

<210> 1

<211> 629

<212> DNA

<213> Pseudoplectania nigrella

<220>

<221> CDS

<222> (10)..(531)

<400> 1

gaattcaaa atg gtc aac ttc acc acc ctc ctc ccg gtt ctt gcc gct ctt  
Met Val Asn Phe Thr Thr Leu Leu Pro Val Leu Ala Ala Leu  
1 5 10

att gga gct gcc aat gcc cac act cgt gtc tac gga ctc tcc gtc aac  
Ile Gly Ala Ala Asn Ala His Thr Arg Val Tyr Gly Leu Ser Val Asn  
15 20 25 30

gat gtc aca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc  
Asp Val Thr Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser  
35 40 45

agt att gcg gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt  
Ser Ile Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val  
50 55 60

cag gtc cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc  
Gln Val Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr  
65 70 75

gac atc cct act ttc act gct act gat gtt cct atc ttc acc aag aag  
Asp Ile Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys  
80 85 90

ccc caa cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct  
Pro Gln Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser  
95 100 105 110

gtt tca ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gcg  
Val Ser Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala  
115 120 125

agc aca atc ccg tca aag ccc aag act ccc gaa gag gtt aat aag tgc 435

Ser	Thr	Ile	Pro	Ser	Lys	Pro	Lys	Thr	Pro	Glu	Glu	Val	Asn	Lys	Cys	
130						135							140			
ctt	gac	gct	gtc	aac	gcc	tgt	att	aca	cag	gcc	cag	agc	tcc	att	gga	483
Leu	Asp	Ala	Val	Asn	Ala	Cys	Ile	Thr	Gln	Ala	Gln	Ser	Ser	Ile	Gly	
145						150						155				
gga	gtt	gtc	aac	ttt	gag	cct	tgc	gag	agc	cag	aga	gct	ctt	tgc	tat	531
Gly	Val	Val	Asn	Phe	Glu	Pro	Cys	Glu	Ser	Gln	Arg	Ala	Leu	Cys	Tyr	
160						165						170				
taggaactgc	aaagaatctg	gggggatgg	agcgagg	ttg	agaggtgg	agaggtgg	gagcgg	gagga								591
gtaggggagg	tgagatgg	agta	gat	taa	gag	cgcccgca										629
<210>	2															
<211>	174															
<212>	PRT															
<213>	Pseudoplectania	nigrella														
<400>	2															
Met	Val	Asn	Phe	Thr	Thr	Leu	Leu	Pro	Val	Leu	Ala	Ala	Leu	Ile	Gly	
1						5				10			15			
Ala	Ala	Asn	Ala	His	Thr	Arg	Val	Tyr	Gly	Leu	Ser	Val	Asn	Asp	Val	
							20			25			30			
Thr	Ser	Ser	Gly	Thr	Ser	Asn	Asp	Lys	Ala	Val	Ala	Ser	Ser	Ser	Ile	
							35			40			45			
Ala	Ala	Val	Asp	Pro	Val	Thr	Ser	Ser	Val	Val	Ala	Ser	Val	Gln	Val	
						50			55			60				
Pro	Asn	Phe	Thr	Ala	Thr	Asp	Val	Pro	Thr	Phe	Thr	Ala	Thr	Asp	Ile	
							65			70			75		80	
Pro	Thr	Phe	Thr	Ala	Thr	Asp	Val	Pro	Ile	Phe	Thr	Lys	Lys	Pro	Gln	
							85			90			95			
Gln	Pro	Ser	Thr	Leu	Leu	Thr	Arg	Thr	Arg	Thr	His	Ala	Ser	Val	Ser	
						100			105			110				
Phe	Val	Ala	Lys	Pro	Ser	Ala	Phe	Ile	Pro	Lys	Pro	Ser	Ala	Ser	Thr	
							115			120			125			
Ile	Pro	Ser	Lys	Pro	Lys	Thr	Pro	Glu	Glu	Val	Asn	Lys	Cys	Leu	Asp	
						130			135			140				

Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val  
145 150 155 160

Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr  
165 170

<210> 3  
<211> 31  
<212> DNA  
<213> Pseudoplectania nigrella

<220>  
<221> misc\_feature Primer NP887U1  
<222> (1)..(31)

<400> 3  
gacatcggtt acggagagtc cgttagacacg a 31

<210> 4  
<211> 34  
<212> DNA  
<213> Pseudoplectania nigrella

<220>  
<221> misc\_feature Primer NP887D1  
<222> (1)..(34)

<400> 4  
acatcctccg gcacacctcaa tgacaaggcc gtcg 34

<210> 5  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Primer PNA2I

<220>  
<221> misc\_feature Primer PNA2I  
<222> (1)..(21)

<400> 5  
gtttccaaact caatttaccc c 21

<210> 6  
<211> 32

```

<212> DNA
<213> Artificial

<220>
<223> Primer NP887Dau1

<220>
<221> misc_feature Primer NP887Dau1
<222> (1)..(32)

<400> 6
ccaaagctt tcatcctccg gcacacctaa tg 32

<210> 7
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer N887Dau2

<220>
<221> misc_feature Primer NP887Dau2
<222> (1)..(32)

<400> 7
gcgaagctta atcttactcc atctcacctc cc 32

<210> 8
<211> 573
<212> DNA
<213> Pseudoplectania nigrella

<220>
<221> CDS
<222> (1)..(570)
<223> Positions 1-57 Candida lipase signal peptide, positions 58-147
      Candida lipase sequence, positions 148-570 P. nigrella CBM
      polypeptide.

<400> 8
atg aag cta ctc tct ctg acc ggt gtg gct ggt gtg ctt gcg act tgc 48
Met Lys Leu Leu Ser Leu Thr Gly Val Ala Gly Val Leu Ala Thr Cys
1 5 10 15

gtt gca gcc act cct ttg gtg aag tgc gca act agt ggc cat tac ggc 96
Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly
20 25 30

ctc gcg agg ccg cct cgg ccc caa cga att ctt gga ata tta agc ttt
Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe 144
35 40 45

```

tca tcc tcc ggc acc tcc aat gac aag gcc gtc gct tct tcc agt att	192
Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile	
50 55 60	
gct gcc gtg gac cct gtg acc agc tcc gtc gta gcc tct gtt cag gtc	240
Ala Ala Val Asp Pro Val Thr Ser Val Val Ala Ser Val Gln Val	
65 70 75 80	
cct aac ttc act gcc act gac gtc ccc act ttt act gcc acc gac atc	288
Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile	
85 90 95	
cct act ttc act gct act gat gtt cct atc ttc acc aag aag ccc caa	336
Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln	
100 105 110	
cag ccc tca act tta ttg acc cgc acc cgt acc cat gcc tct gtt tca	384
Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser	
115 120 125	
ttc gtc gct aag ccc tcc gct ttt att ccc aag cct tcc gct agc aca	432
Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr	
130 135 140	
atc ccg tca aag ccc aag act ccc gaa gag gtt aat aag tgc ctt gac	480
Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp	
145 150 155 160	
gct gtc aac gcc tgt att aca cag gcc cag agc tcc att gga gga gtt	528
Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val	
165 170 175	
gtc aac ttt gag cct tgc gag agc cag aga gct ctt tgc tat tag	573
Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr	
180 185 190	

<210> 9  
 <211> 190  
 <212> PRT  
 <213> Pseudoplectania nigrella  
  
 <400> 9

Met Lys Leu Leu Ser Leu Thr Gly Val Ala Gly Val Leu Ala Thr Cys  
 1 5 10 15

Val Ala Ala Thr Pro Leu Val Lys Cys Ala Thr Ser Gly His Tyr Gly  
 20 25 30

Leu Ala Arg Pro Pro Arg Pro Gln Arg Ile Leu Gly Ile Leu Ser Phe  
 35 40 45

Ser Ser Ser Gly Thr Ser Asn Asp Lys Ala Val Ala Ser Ser Ser Ile  
50 55 60

Ala Ala Val Asp Pro Val Thr Ser Ser Val Val Ala Ser Val Gln Val  
65 70 75 80

Pro Asn Phe Thr Ala Thr Asp Val Pro Thr Phe Thr Ala Thr Asp Ile  
85 90 95

Pro Thr Phe Thr Ala Thr Asp Val Pro Ile Phe Thr Lys Lys Pro Gln  
100 105 110

Gln Pro Ser Thr Leu Leu Thr Arg Thr Arg Thr His Ala Ser Val Ser  
115 120 125

Phe Val Ala Lys Pro Ser Ala Phe Ile Pro Lys Pro Ser Ala Ser Thr  
130 135 140

Ile Pro Ser Lys Pro Lys Thr Pro Glu Glu Val Asn Lys Cys Leu Asp  
145 150 155 160

Ala Val Asn Ala Cys Ile Thr Gln Ala Gln Ser Ser Ile Gly Gly Val  
165 170 175

Val Asn Phe Glu Pro Cys Glu Ser Gln Arg Ala Leu Cys Tyr  
180 185 190